



Berufungsvorträge
„Dynamical Systems in Biomathematics“

Die Berufungsvorträge schließen folgende Punkte mit ein:

- Didaktischer Vortrag (20 Minuten)
- Fragen/Pause (10 Minuten)
- Wissenschaftlicher Vortrag (45 Minuten)
- Fragen/Pause (15 Minuten)
- Kommissionelles Hearing -
(Dekanatsbesprechungszimmer, 11. Stock)

Donnerstag, 19. Dezember 2019, Hörsaal 2

Franziska Michor
(Harvard University)

14:30 Uhr: Didaktischer Vortrag

„Topics in dynamical systems modeling of evolution and ecology“

In this talk, I will give a sample of recent teaching for applied mathematics majors at Harvard University.

15:15 Uhr: Wissenschaftlicher Vortrag

„Dynamical systems modeling of human brain cancer“

Brain cancer is among the deadliest malignancies in people. In this talk, I will discuss recent research applying dynamical systems modeling to human brain cancer treatment response and optimization.

Donnerstag, 23. Jänner 2020, Hörsaal 16

Emmanuel Schertzer
(Sorbonne Université)

09:00 Uhr: Didaktischer Vortrag

„A standard model in population genetics: The Wright-Fisher model“

I will introduce one of the simplest models in population genetics: the Wright-Fisher model. The Wright-Fisher model describes the random fluctuations of an allele's frequency inside a neutral population (i.e., in the absence of natural selection) and in the absence of any demographic effects. I will focus on the description of the genealogy obtained by first sampling individuals in an extant population and then tracing backward in time their ancestral lineages (the celebrated Kingman coalescent).

09:30 Uhr: Wissenschaftlicher Vortrag

„Some extensions of the Wright-Fisher model“

In the second part of the talk, I will discuss some extensions of the previous model. Arguably, the Wright-Fisher model is very simplistic and does not take into account many of the evolutionary forces which could have an impact on today's genetic diversity. First, this model is neutral in the sense that individuals are assumed to be exchangeable in the face of death and reproduction. Secondly, populations are assumed to be panmictic and demographic effects are ignored. Thirdly, the previous models are quite restrictive since they only model the evolution at a single locus, whereas recombination is known to introduce some non-trivial correlation on the evolutionary histories along the genome.

Going beyond those restrictions is known to be a serious challenge and a large fraction of my talk will be dedicated to some of my contributions in this direction. I will focus mainly on two models that are easy to describe but offer some challenging mathematical questions. The first model is the nested Kingman coalescent model which arises in the context of biological systems where replication occurs at multiple levels. (In phylodynamics: pathogens proliferate inside their hosts and propagate from host to host; In macro-evolution: gene lineages are nested inside a larger species tree.) The second model is the ancestral recombination graph which aims at describing the correlation between the evolutionary histories at distinct loci along the genome.



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Donnerstag, 23. Jänner 2020, Hörsaal 5

**Bärbel Finkenstädt Rand
(University of Warwick)**

15:00 Uhr: Didaktischer Vortrag

„Parameter Estimation for Biological Systems“

The mathematical equations used to develop biological systems often are complex so that, except for the most simple cases, we have to resort to numerical simulations for the purpose of prediction. This, however, requires us to assign specific values to the parameters that describe the properties of the system (for example, half-lives and kinetic rates in biochemical systems, birth-and death-rates in population models). The task of parameter estimation from data is also called an ‘inverse problem’ and has become increasingly important with the amount of experimental data now becoming available. I will introduce likelihood based estimation, including Bayesian inference, and a simple simulation based method to assess the properties of the resulting parameter estimator.

15:30 Uhr: Wissenschaftlicher Vortrag

„Inference for Circadian Pacemaking“

Organisms have evolved an internal biological clock which allows them to temporally regulate and organize their physiological and behavioral responses to cope in an optimal way with the fundamentally periodic nature of the environment. It is now well established that the molecular genetics of such rhythms within the cell consist of interwoven transcriptional-translational feedback loops involving about 15 clock genes, which generate circa 24-h oscillations in many cellular functions at cell population or whole organism levels. We will present statistical methods and modelling approaches that address newly emerging large circadian data sets, namely spatio-temporal gene expression in SCN neurons and rest-activity actigraph data obtained from non-invasive e-monitoring, both of which provide unique opportunities for furthering progress in understanding the synchronicity of circadian pacemaking and address implications for monitoring patients in chronotherapeutic healthcare.

Freitag, 24. Jänner 2020, Seminarraum 5

**Klemens Fellner
(Universität Graz)**

09:00 Uhr: Didaktischer Vortrag

„Die Macht des Kollektivs oder die Hölle, das sind die anderen?“

Ein kleiner Einblick in die facettenreiche Welt des kollektiven Verhaltens von Individuen und deren mathematischer Modellierung als Teil eines Vorlesungsblocks rund um die Stichworte Schwarmverhalten, Keller-Segel, Partikelsysteme vs. Kontinuumsbeschreibung.

09:30 Uhr: Wissenschaftlicher Vortrag

„Bio-chemical reaction-diffusion type systems and their analysis“

Exemplified by mathematical models for stem-cell division, prion dynamics and lipolysis, we provide an overview over recent progress on the analysis and large-time behaviour of reaction-diffusion type models.



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Montag, 27. Jänner 2020, Hörsaal 17

**Maria Vittoria Barbarossa
(Universität Heidelberg)**

09:00 Uhr: Didaktischer Vortrag

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09:30 Uhr: Wissenschaftlicher Vortrag

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Montag, 27. Jänner 2020, Hörsaal 16

**Christian Hilbe
(Max-Planck-Institute for Evolutionary Biology, Plön)**

15:00 Uhr: Didaktischer Vortrag

„Dynamical systems and Lyapunov stability“

In this lecture I will review some basic notions of dynamical systems. In particular, I will formally introduce dynamical systems for both discrete and continuous time. Moreover, I will discuss different notions of stability of fixed points.

15:30 Uhr: Wissenschaftlicher Vortrag

„The dynamics of direct and indirect reciprocity“

Direct and indirect reciprocity are two key explanations for the evolution of cooperation. The former is based on direct experience. It posits that we cooperate with those who have cooperated with us in the past. The latter is based on public standings, positing that we cooperate with those who have a cooperative reputation (even if we did not benefit directly). Models of reciprocity describe how reputations change over time, depending on which actions individuals take, which information they have about each other, and which social norms (or strategies) they employ.

The talk consists of two parts. The first part will provide some background on previous models of direct and indirect reciprocity, and the kinds of dynamical systems they give rise to. While in previous work each mode of reciprocity was studied in isolation, in the second part I will introduce a model that can be used to study the joint evolution of direct and indirect reciprocity. If time permits, I will also give a brief outlook on future work.